

quantitatively. We applied this technique to the analysis of exoprotein from SDSE.

Methods: The SDSE strains used in this study were 1 reference strain H46A and 23 clinical isolates from patients with invasive disease in Japan. The bacteria were cultured in brain heart infusion broth containing 0.3% yeast extract for 16 hours. After bacterial culture supernatant was prepared with TCA-acetone concentration, aliquots of the samples were loaded onto 7cm Immobiline DryStrip gels (pH 3 to 10). The first-dimensional electrophoresis conditions and second-dimensional SDS-PAGE separation were performed. The gels were stained with coomassie brilliant blue. Those proteins in the spots were also identified by peptide mass mapping analysis.

Results: We identified 25 spots of exoprotein in SDSE H46A strain by 2-DE analysis. Furthermore we found various amount of Streptokinase among 23 clinical strains by 2-DE analysis and we could also divide 3 exoprotein patterns by the production of Streptokinase in 24 SDSE.

Conclusion: Our study suggests that the 2-DE analysis is useful for categorizing the exoprotein patterns, especially Streptokinase, in SDSE strains.

OL-016 The turn-around-times (TATs) of BacT/ALERT 3D™ and VersaTREK™

C. Deocaris^{1,2*}, B. Dagumol³, H. Pascual³, R. Dela Rosa⁴, E.M. Abendano², L. Manganip², R. De Mesa-Rodriguez². ¹Department of Biology, CAS, UP Manila, ²Inst. Ophthalmology, NIH, UP Manila, ³Department of Pathology, Armed Forces of the Philippines Medical Center (AFPMC), ⁴Infectious Ward, Armed Forces of the Philippines Medical Center (AFPMC), Philippines

We compared the Turn-Around-Times (TATs) of two competing automated microbial detection systems BacT/ALERT 3D™ (BACT) (bioMérieux, Inc., Durham, NC) and the VersaTREK™ (VTRK) (TREK Diagnostic Systems, Cleveland, OH) through the blood culture analysis results of the Armed Forces of the Philippines Medical Center (Quezon City, Philippines) from January-December 2010. Blood cultures were positive at the rate of 182/888 (25.78%) for BTAC and 159/898 (21.54%) for VTRK. The positivity rate for the two systems was not significantly different ($\chi^2 = 2.2151$, $df = 1$, $p = 0.1367$). Organisms that grew in the blood culture bottles were identified as *Staphylococcus aureus* ($n = 36$), *Staphylococcus epidermidis* ($n = 119$), *Enterobacter aerogenes* ($n = 36$), *Enterobacter agglomerans* ($n = 3$), *Enterobacter cloacae* ($n = 5$), *Escherichia coli* ($n = 21$), *Proteus spp* ($n = 21$), *Acinetobacter spp* ($n = 61$), *Alcaligenes spp.* ($n = 24$) and *Pseudomonas aeruginosa* ($n = 6$).

Our data revealed the TAT for BTAC to detect blood pathogens is 23.69 ± 14.85 hours and 22.24 ± 12.77 hours for VTRK. The difference between the two systems was not significant ($z = 0.9734$, $p\text{-value} = 0.3304$). The TAT of systems is not affected by the strain type of organism detected ($F = 1.6988$, $df = 9$, $p = 0.0882$). On the otherhand, methicillin resistance in *S. aureus* and *S. epidermidis* did affect the TAT of detection ($F = 0.0806$, $df = 1$, $p = 0.7782$ and $F = 1.9329$, $df = 1$, $p = 0.161$ respectively).

From our findings, we conclude that the BTAC and VTRK systems are comparable in terms of the positivity rate and TAT for the detection of bloodstream bacterial infections. Likewise, the antibiotic resistance of the organisms did affect the TAT of the systems.

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PL-003 Seroepidemiology of *Anaplasma phagocytophilum* among farm worker populations in the Tianjin area during 2007–2009

C.W. Liang^{1,2}, Y. Zhang³, J.B. Zhao¹, Z.L. Zhang³, H.L. Yu², J.Y. Yin³, S.W. Wang², J. Lv³, L.J. Zhang^{2*}. ¹School of Public Health, Harbin Medical University, ²National Institute of Communicable Disease Control and Prevention, Chinese Center for Disease Control and Prevention, Beijing 102206, ³Tianjin Municipal Center for Disease Control and Prevention, Tianjin 300011, China

Objective: Spotted fever, Human granulocytic anaplasmosis (HGA) and monocytic ehrlichiosis (HME) are worldwide tick-borne rickettsial diseases (TBRD) caused by the obligate intracellular bacteria spotted fever group rickettsiae (SFGR), *Anaplasma phagocytophilum* and *Ehrlichia chaffeensis* respectively. In 2006, the seroepidemiologic data from Tianjin area demonstrated average infection prevalences in farm population as 8.8% similar to rates among serosurveys in North America and Europe. In this study, we describe a continuous seroprevalence investigation of *A. phagocytophilum* in Tianjin areas from 2007 to 2009.

Methods: Field epidemiological surveys were performed in 8 districts of Tianjin and 886 farmers were randomly recruited and their serum samples were collected to detect the specific IgG antibodies of *A. phagocytophilum* by micro-indirect immunofluorescence (IFA).

Results: The IgG antibody positive rates of *A. phagocytophilum* increased from 8.8% in 2006 to 59.2% in 2009 while *E. chaffeensis* had an increase from 0.0% in 2006 to 4.4% in 2009. However, spotted fever group rickettsiae decreased from 1.6% in 2007 to 0.0% in 2009.

Conclusion: Infections of both *A. phagocytophilum* and *E. chaffeensis* in farmers from Tianjin areas were popular and the antibody positive rates of *A. phagocytophilum* and *E. chaffeensis* increased annually. Differential diagnosis for rickettsial diseases in clinical practice and watch out for outbreaks of anaplasmosis and ehrlichiosis in rural areas should be emphasized. Further investigation on vectors and hosts of these rickettsioses in Tianjin areas should also be performed.

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OL-017 Aquaporin water channel AgAQP1 in the malaria vector mosquito *Anopheles gambiae* during blood feeding and humidity adaptation

K. Liu^{1*}, H. Tsujimoto¹, S.-J. Cha¹, P. Agre¹, J. Rasgon¹. ¹Johns Hopkins Malaria Research Institute, Baltimore, MD, USA

Background: Altered patterns of malaria endemicity reflect changes in the feeding behavior and climate adaptation of *Anopheles gambiae* mosquito, which require fast transmembrane water movement. We anticipate that AQP water channels play important role in the physiology of this malaria mosquito vector.